



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Patent

In re patent application of: AGUERA et al.

Serial No.: 09/367,496

Examiner: Rawlings

Filed: August 17, 1999

Art Unit: 1642

For: USE OF ULIP PROTEINS IN THE DIAGNOSIS AND THERAPY OF CANCERS AND PARANEOPLASTIC... Docket #: P06473US0/BAS

**STATEMENT UNDER 37 CFR §1.821**

Commissioner for Patents  
Washington, D.C.

S I R:

I hereby certify in accordance with 37 CFR §1.821(f) that the content of the enclosed paper sequence listing and computer readable form of the sequence listing are the same. In accordance with 37 CFR §1.821(g), I hereby certify that the enclosed submission contains no new matter.

Respectfully submitted,

Date: March 25, 2002

By:   
B. Aaron Schulman  
Registration No. 31,877

LARSON & TAYLOR PLC  
Transpotomac Plaza  
1199 North Fairfax Street, Suite 900  
Alexandria, Virginia 22314  
(703) 739-4900

## alignement des cDNA humains Ulip1-4

hUlip-1  
hUlip-2  
hUlip-3  
hUlip-4

ATGTCCTACCAAGGCAAGAAGAACATCCCGGGATCACGAGTGACCGTCT  
ATGTCTTATCAGGGGAAGAAAATATTCACGCATCACGAGCGATCGTCT  
ATGTCGTACCAGGGCAAGAAGAGCATCCCGCACATCACGAGTGACCGACT  
ATGTCCTTCCAGGGCAAGAAAAGCATCCCCGGATCACGAGTGACCGCCT  
\*\*\*\*\*

hUlip-1  
hUlip-2  
hUlip-3  
hUlip-4

CCTTATCAAGGGAGGCAGAATCGTCAATGATGATCAGTCCTTTATGCTG  
TCTGATCAAAGGAGGTAAATTTGTTAATGATGACCACTCGTTCTATGCAG  
CCTCATCAAAGGTGGACGGATCATCAACGATGACCAATCCCTTTATGCTG  
TCTGATCAGAGGTGGGAGGATCGTGAATGACGACCACTCCTTTACGCTG  
\*\*\*\*\*

hUlip-1  
hUlip-2  
hUlip-3  
hUlip-4

ATATTTACATGGAAGATGGCTTAATAAAACAAATTGGAGACAATCTGATT  
ACATATACATGGAAGATGGGTTGATCAAGCAAATAGGAGAAAATCTGATT  
ACGTCTACCTGGAGGATGGACTTATCAAACAAATAGGAGAGAACTTAATC  
ATGTGCACGTGGAAGATGGCTTGATAAAACAAATCGGAGAAAACCTCATC  
\*\*\*\*\*

hUlip-1  
hUlip-2  
hUlip-3  
hUlip-4

GTTCTGGAGGAGTGAAGACCATTGAAGCCAATGGGAAGATGGTGATCCC  
GTGCCAGGAGGAGTGAAGACCATCGAGGCCACTCCCGGATGGTGATCCC  
GTTCTGGTGGAGTGAAGACCATTGAAGCCAACGGGCGGATGGTTATTC  
GTCCCTGGGGGCATCAAGACCATTGACGCCACGGCCTGATGGTCCTTC  
\*\*\*\*\*

hUlip-1  
hUlip-2  
hUlip-3  
hUlip-4

TGGAGGCATCGATGTCCATACTCACTTCCAGATGCCATATAAGGGAATGA  
CGGAGGAATTGACGTCCACACTCGTTCCAGATGCCATGATCAGGGAATGA  
CGGAGGTATTGATGTCAACAGTACCTGCAGAGCCCTCCAGGGGATGA  
TGGTGGCGTTGACGTCCACACAAGGCTGCAGATGCCTGTCTGGGCATGA  
\*\*\*\*\*

hUlip-1  
hUlip-2  
hUlip-3  
hUlip-4

CCACAGTAGATGACTTCTTCCAAGGGACAAAGGCGGCCTTAGCAGGTGGC  
CGTCTGCTGATGATTTCTTCCAAGGAACCAAGGCGGCCCTGGCTGGGGGA  
CTGCGGCTGATGACTTCTTCCAAGGGAACAGGCGGCACTGGTGGGCGGG  
CACCAGCTGACGACTTCTGTGAGGGCACCAGGCGCTAGCAGGAGGA  
\*\*\*\*\*

hUlip-1  
hUlip-2  
hUlip-3  
hUlip-4

ACCACCATGATCATTGACCATGTGGTGCCTGAGCCTGAGTCCAGCCTGAC  
ACCACTATGATCATTGACCACGTTGTTCTGAGCCTGGGACAAGCCTGCT  
ACCACGATGATCATTGACCATGTTGTTCTGAACCTGGGTCCAGCCTACT  
ACCACCATGATCTTGGACACGTTCTTCCCGACAGGGGTGTGAGCCTGCT  
\*\*\*\*\*

hUlip-1  
hUlip-2  
hUlip-3  
hUlip-4

TGAGGCCTATGAGAAATGGAGAGAGTGGGCTGATGGGAAGAGTTGCTGTG  
CGCTGCCCTTGACCAAGTGGAGGGAATGGGCCGACAGCAAGTCTGCTGTG  
GACCTCTTTCGAGAAGTGGCACGAAGCAGCTGACACCAATCCTGCTGTG  
GGCGGCCTACGAGCGGTGGCGGGAGCGGGCGGACAGCGGCCCTGCTGCG  
\*\*\*\*\*

hUlip-1  
hUlip-2  
hUlip-3  
hUlip-4

ACTATGCCCTGCATGTGGACATCACCCACTGGAATGACAGCGTCAAGCAG  
ACTACTCTCTGCATGTGGACATCAGCGAGTGGCATAAGGGCATCCAGGAG  
ATTACTCCCTCCACGTGGACATCACAAGCTGGTACGATGGCGTTCGGGAG  
ACTACTCCCTGCACGTGGACATCACCCATGGCATGAGAGCATCAAGGAG  
\*\*\*\*\*

hUlip-1  
hUlip-2  
hUlip-3  
hUlip-4

GAAGTGCAGAACCTCATCAAGGACAAAGGGGTAACTCCTTCATGGTTTA  
GAGATGGAAGCGCTTGTGAAGGATCACGGGGTAAATTCCTTCCTCGTGA  
GAGCTGGAGGTGCTGGTGCAGGACAAAGCGTCAATTCCTTCCAAGTCTA  
GAGCTGGAGGCCCTGGTCAAGGAGAGGGTGTGAACCTCCTTCCTGCTCT  
\*\*\*\*\*

hUlip-1  
hUlip-2  
hUlip-3  
hUlip-4

TATGGCTTATAAGGATTTGTATCAAGTATCTAACACAGAGCTCTATGAGA  
CATGGCTTTCAAAGATCGCTTCCAGCTAACGGATTGCCAGATTATGAAG  
CATGGCCTATAAGGATGTCTACCAATGTCCGACAGCCAGCTCTATGAAG  
CATGGCATAACAAGGACCGGTGCCAGTGCAGCGACAGCCAGATGTACGAGA  
\*\*\*\*\*

hUlip-1  
hUlip-2  
hUlip-3  
hUlip-4

TCTTCACCTGCCTGGGAGAGCTGGGGGCCATTGCTCAAGTTCATGCTGAG  
TACTGAGTGTGATCCGGGATATTGGCGCCATAGCCCAAGTCCACGCAGAA  
CCTTTACCTTCTTAAGGGCCTGGGAGCTGTGATCTTGGTCCATGCAGAA  
TCTTCAGCATCATCCGGGACCTGGGGGCCTTGGCCAGGTGCACGCTGAG  
\*\*\*\*\*

hUlip-1  
hUlip-2  
hUlip-3  
hUlip-4

AATGGGGATATCATTGCCAGGAGCAAACCCGCATGTTGGAAATGGGGAT  
AATGGCGACATCATTGCAGAGGAGCAGCAGAGGATCCTGGATCTGGGCAT  
AATGGAGATTTGATAGCTCAGGAACAAAGCGGATCCTGGAGATGGGCAT  
AACGGGGACATCGTGGAGGAGGAGCAGAAGCGGTTGCTGGAGCTCGGCAT  
\*\*\*\*\*

hUlip-1  
hUlip-2  
hUlip-3  
hUlip-4

AACTGGCCCAGAAGGCCATGTACTGAGCAGGCCAGAAGAGCTGGAAGCTG  
CACGGGCCCCGAGGGACATGTGCTGAGCCGACCTGAGGAGGTGAGGCCG  
CACGGGTCCCGAGGGCCATGCCCTGAGCAGACCTGAAGAGCTGGAGGCCG  
CACTGGCCCCGAGGGCCACGTGCTCAGCCACCCCGAGGAGGTGAGGCTG  
\*\*\*\*\*

hUlip-1  
hUlip-2  
hUlip-3  
hUlip-4

AGGCTGTGTTCCGTGCCATCACCATTGCCAGCCAAACCAATTGCCCTCTC  
AAGCCGTGAATCGTGCCATCACCATCGCCAACCAAGACCAACTGCCCGCTG  
AGGCGGTGTTCCGGGCCATCACCATTGCGGGCCGGATCAACTGCCCTGTG  
AGGCGGTGTACCGAGCTGTACCATCGCCAAGCAGGCAAACTGCCCGCTG  
\*\*\*\*\*

hUlip-1  
hUlip-2  
hUlip-3  
hUlip-4

TACGTACAAAGGTTCATGAGCAAGAGTGCAGCTGACCTCATCTCACAAGC  
TATATCACCAAGGTGATGAGCAAAAGCTCTGCTGAGGTCACTGCCAGGC  
TACATCACCAAGGTTCATGAGCAAGAGTGCAGCCGACATCATCGCTCTGGC  
TACGTACCAAGGTGATGAGCAAGGGGCGCGCCGACCCATCGCTCAGGC  
\*\*\*\*\*

hUlip-1  
hUlip-2  
hUlip-3  
hUlip-4

CAGGAAAAAGGAAATGTAGTCTTTGGTGAGCCCATCACTGCCAGCCTCG  
ACGGAAGAAGGGAAGTGTGGTGATGGCGAGCCCATCACTGCCAGCTTGG  
CAGGAAGAAAGGGCCCTAGTTTTTGGAGAGCCCATTGCCGCCAGCCTGG  
CAAGCGCAGAGGGGTGGTGTGTTTGGGAGCCCATACCGCCAGCCTGG  
\*\*\*\*\*

hUlip-1  
hUlip-2  
hUlip-3  
hUlip-4

GCATAGATGGAACCCATTATTGGAGCAAGAAGTGGGCCAAGGCGGCTGCA  
GAACGGACGGCTCCCATTACTGGAGCAAGAAGTGGGCCAAGGCTGCTGCC  
GGACCGATGGCACCCATTACTGGAGCAAGAAGTGGGCCAAGGCTGCGGCG  
GCACCGACGGTTCACACTACTGGAGCAAGAAGTGGGCCAAGGCCGAGCC  
\*\*\*\*\*

hUlip-1  
hUlip-2  
hUlip-3  
hUlip-4

TTTGTGACATCCCCACCCCTGAGCCCTGACCCAACCTACTCCGGACTACAT  
TTTGTACCTCCCCACCCCTGAGCCCTGATCCAACCACTCCAGACTTTCT  
TTCGTGACTTCCCTCCCTGAGCCCGGACCCATACCAGGCCGACTACTT  
TTCGTACATCACCCTGTCAACCCAGACCCACCCAGGCAGACCACT  
\*\*\*\*\*

hUlip-1  
hUlip-2  
hUlip-3  
hUlip-4

CAACTCCTTGCTGGCCAGCGGGGATCTGCAGCTATCTGGGAGTGCCCACT  
CAACTCCTTGCTGTCTGTGGAGACCTCCAGGTACGCGGCAGTGCCCACT  
GACCTCCCTACTGGCCTGTGGGGACTTGCAAGTACAGGCAGCGGCCACT  
CACTGTCTGTCTCCAGCGGGGACCTCCAGGTGACAGGCAGCGGCCACT  
\*\*\*\*\*

hulip-1  
hulip-2  
hulip-3  
hulip-4

GCACCTTCAGCACTGCCAGAAAGCAATTGGGAAGGACAACCTTCACAGCC  
GCACGTTTTAACTGCCAGAAAGGCTGTAGGAAAGGACAACCTTCACCCTG  
GTCCCTACAGCACTGCCAGAAAGGCGGTGGGCAAGGACAACCTTACCCTG  
GCACCTTCACCCTGCCAGAAAGGCTGTGGGCAAGGACAACCTTCGCGCTG  
\* \* \* \* \*

hulip-1  
hulip-2  
hulip-3  
hulip-4

ATTCCCTGAGGGCACCAATGGTGTGGAGGAGCGGATGTCTGTCTCTGGGA  
ATTCCGGAGGGCACCAATGGCACTGAGGAGCGGATGTCCGTCTCTGGGA  
ATCCCCGAGGGTGTCAACGGGATAGAGGAGCGGATGACCGTCGTCTGGGA  
ATCCCCGAGGGCACCAACGGCATTGAGGAGCGCATGTCTGTCTGGGA  
\* \* \* \* \*

hulip-1  
hulip-2  
hulip-3  
hulip-4

CAAGGCTGTGGCCACAGGGAAAATGGACGAAAACCAAGTTCGTGGCTGTGA  
CAAGGCTGTGGTCACTGGGAAGATGGATGAGAACCAGTTGTGGCTGTGA  
CAAGGCGGTGGCTACTGGCAAATGGATGAGAACCAGTTGTCTGTCTGA  
GAAATGTGTGGCTCTGGGAAGATGGACGAGAATGAGTTCGTGGCGGTGA  
\* \* \* \* \*

hulip-1  
hulip-2  
hulip-3  
hulip-4

CAAGCACAAACGCTGCCAAGATCTTCAACCTGTATCCCCGCAAGGGAAGA  
CCAGCACCAATGCAGCCAAAGTCTTCAACCTTTACCCCCGGAAGGCCGC  
CCAGCACCAATGCAGCCAAAGTCTTCAACCTGTACCCAAGGAAAGGGCGG  
CCAGTACAAATGCTGCCAAAATCTTCAATTTTACCCAAGGAAAGGGCGA  
\* \* \* \* \*

hulip-1  
hulip-2  
hulip-3  
hulip-4

ATATCTGTGGGTTCTGACAGCGACCTCGTCATCTGGGATCCAGATGCTGT  
ATTGCTGTGGGATCCGATGCCGACCTGGTCTCTGGGACCCCGACAGCGT  
ATTGCCGTGGGCTCGGATGCCGACCTGGTCTCTGGGACCCCGACAAGTT  
GTGGCTGTGGGCTCTGACGCTGACCTGGTCTATGGAACCCCAAGGCCAC  
\* \* \* \* \*

hulip-1  
hulip-2  
hulip-3  
hulip-4

GAAGATCGTCTCTGCCAAGAACCACAGTCTGCGGCAGAGTACAACATCT  
TAAAACCATCTCTGCCAAGACACACAACAGCTCTCTCGAGTACAACATCT  
GAAGACCATAACAGCCAAAGTCAAGTCCGCGGTGGAGTACAACATCT  
CAAGTCATCTCTGCCAAGACCCACAATCTGAACGTGGAGTACAACATCT  
\* \* \* \* \*

hulip-1  
hulip-2  
hulip-3  
hulip-4

TTGAAGGGATGGAGCTGCCGCGGGCTCCTCTGGTTGTCTATCTGCCAGGGC  
TTGAAGGCATGGAGTGCCGCGGGCTCCCCACTGGTGGTCTATCAGCCAGGGG  
TCGAGGGTATGGAGTGCCACGGCTCCCCACTAGTGGTCTATCAGCCAGGGC  
TCGAGGGAGTGCAGTGCCGCGGGAGCGCCTGCCGTGGTCTAAGTCAAGGGC  
\* \* \* \* \*

hulip-1  
hulip-2  
hulip-3  
hulip-4

AAGATCATGCTGGAAGATGGCAACCTGCACGTGACCCAGGGGGCTGGCCG  
AAGATTGCTCTGGAGGACGGCACCTGCATGTCAACGAAGGCTCTGGACG  
AAGATCGTCTTTGAAGACGGAAACATCAACGTCAACAAGGGCATGGGCGG  
CGAGTGGCGCTGGAGGACGGGAAGATGTTGTACCCCGGGGGCGGGCCG  
\* \* \* \* \*

hulip-1  
hulip-2  
hulip-3  
hulip-4

CTTCATACCCTGCAGCCCGTTCTCCGACTATGTCTACAAGCGCATTAAAG  
CTACATTCCCCGGAAGCCCTTCCCTGATTTTGTCTACAAGCGTATCAAGG  
CTTCATTCCGCGGAAGGCGTTCCCGGAGCACCTGTACCAGCGCGTCAAAA  
CTTCGTCCTCTCGGAAAACATTCCCGGACTTTGTCTACAAGAGGATCAAG  
\* \* \* \* \*

hulip-1  
hulip-2  
hulip-3  
hulip-4

CACGGAGGAAGATGGCAGACCTGCATGCCGTCCCAAGGGGCATGTACGAT  
CAAGGAGCAGGCTGGCTGAGCTGAGAGGGGTTCCCTCGTGGCCTGTATGAC  
TCAGGAATAAGGTTTGTGATTGCAAGGGGTTTCAGGGGCATGTATGAC  
CTCGCAACAGGCTGGCGGAGATCCACGGTGTGCCCGTGGGCTGTATGAC  
\* \* \* \* \*

X

hUlip-1 GGGCCTGTGTTTGACCTGACCACCACCCCAAAGGTGGCACCCTCGCAGG  
hUlip-2 GGACCTGTGTGTGAAGTGTCTGTGACGCCCCAAGACAGTCACTCCAGCCTC  
hUlip-3 GGTCTGTGTACGAGGTACCAGCTACACCCAAATATGCAACTCCCGCTCC  
hUlip-4 GGGCCCGTCCACGAGGTGATGGTGCCTGCCAAGCCAGGGAGTGGCGCTCC  
\* \* \* \* \*

hUlip-1 CTCTGCTCGGGGCTCTCCTACT---CGGCCGAACCCACCTGTGAGGAATC  
hUlip-2 CTCGGCCAAGACGTCTCCTGCCAAGCAGCAGGCCCCACCTGTCCGGAACC  
hUlip-3 TTCAGCCAAATCTTCGCCTTCTAAACACCAGCCCCACCCATCAGAAACC  
hUlip-4 GGCCCGCGCGTCTCTGCCCAGGCAAGATCTCCGTGCCTCTCTGTGCGCAACC  
\* \* \* \* \*

hUlip-1 TTCATCAGTCGGGATTTAGCCTGTGAGGCACCCAAGTGGATGAGGGGGTT  
hUlip-2 TGCACCACTCTGATTTCAGTTTGTCTGGTGCTCAGATTGATGACAACATT  
hUlip-3 TCCACCAGTCCAACTTCAGCTTATCAGGTGCCCAGATAGATGACAAACAT  
hUlip-4 TACATCAGTCGGGGTTTACGCTATCTGGGTCTCAGGCTGATGACCACATC  
\* \* \* \* \*

hUlip-1 C---GCTCAGCCAGCAAGCGCATCGTGGCCCCCCCAGGCGGCCGTCTTAA  
hUlip-2 CCCCCGCCGACCCACCCAGCGTATCGTGGCGCCCCCGGTGGCCGTGCCAA  
hUlip-3 CCGAGGCGCACCCGCCACCGCATCGTGGCGCCCCCTGGTGGCCGCTCCAA  
hUlip-4 GCGCGACGCACAGCACAGAAGATCATGGCACCACTGGCGGCCGCTCCAA  
\* \* \* \* \*

hUlip-1 TATCACATCTCTGAGTTAA  
hUlip-2 CATCACCAGCCTGGGCTAG  
hUlip-3 CATCACCAGCCTCGGTTGA  
hUlip-4 CATCACCTCTCTCTCCTAG  
\* \* \* \*

Sequences (U1:U2) Aligned. Score: 68.7682  
Sequences (U1:U3) Aligned. Score: 67.0169  
Sequences (U1:U4) Aligned. Score: 64.6235  
Sequences (U2:U3) Aligned. Score: 70.1571  
Sequences (U2:U4) Aligned. Score: 69.0518  
Sequences (U3:4) Aligned. Score: 65.2705